SEQUENCE LISTING

<110>	Jenuwein, Thomas Laible, Gotz O'Carroll, Donal Eisenhaber, Frank Rea, Stephen			
<120>	Chromatin-Regulator Gene	s		
<130>	0652.1670001			
<140> <141>	US 09/589,892 2000-06-09			
<150> <151>	US 08/945,988 1997-11-10		•	
<150> <151>	PCT/EP96/01818 1996-05-02			
<150> <151>	DE 195 16 776.7 1995-05-10		·	
<160>	21		•	
<170>	PatentIn version 3.2			
<210><211><211><212><213>	1 2600 DNA Homo sapiens			
<220> <221> <222>	5'UTR (1)(89)		·	
<220> <221>	CDS			
<222>	(90) (2330)			
<220>	2.44000			
<221> <222>	3'UTR (2331)(2600)			
<400>	1			•
aggcagt	oga geceeggegg eggeggegge	c ggcgcgcggg	ggcgacgcgc ggga	acaacg 60
cgagtcg	ggcg cgcgggacga agaataatc		act ggg aag aaa Thr Gly Lys Lys 5	
	g gga cca gtt tgt tgg cgg s Gly Pro Val Cys Trp Arg 15			
	g aga cag ctc aag agg ttc Arg Gln Leu Lys Arg Phe 30			
atg ttt	agt tcc aat cgt cag aaa	att ttg gaa	aga acg gaa atc	tta 257

Met	Phe	Ser	Ser	Asn 45	Arg	Gln	Lys	Ile	Leu 50	Glu	Arg	Thr	Glu	Ile 55	Leu	
aac Asn	caa Gln	gaa Glu	tgg Trp 60	aaa Lys	cag Gln	cga Arg	agg Arg	ata Ile 65	cag Gln	cct Pro	gtg Val	cac His	atc Ile 70	ctg Leu	act Thr	305
						Gly 999										353
						gtc Val 95										401
gct Ala 105	tca Ser	gta Val	ccc Pro	ata Ile	atg Met 110	tat Tyr	tct Ser	tgg Trp	tct Ser	ccc Pro 115	cta Leu	cag Gln	cag Gln	aat Asn	ttt Phe 120	449
						gtt Val										497
gaa Glu	gtt Val	tta Leu	gat Asp 140	cag Gln	gat Asp	ggt Gly	act Thr	ttc Phe 145	att Ile	gaa Glu	gaa Glu	cta Leu	ata Ile 150	aaa Lys	aat Asn	545
						Gl ^A aaa										593
gaa Glu	att Ile 170	ttt Phe	gtg Val	g ag Glu	ttg Leu	gtg Val 175	aat Asn	gcc Ala	ctt Leu	ggt Gly	caa Gln 180	tat Tyr	aat Asn	gat Asp	gat Asp	641
						gac Asp										689
aaa Lys	gat Asp	ctg Leu	gag Glu	gat Asp 205	cac His	cga Arg	gat Asp	gat Asp	aaa Lys 210	gaa Glu	agc Ser	cgc Arg	cca Pro	cct Pro 215	cgg Arg	737
						att Ile										785
gat Asp	aag Lys	ggc Gly 235	aca Thr	gca Ala	gaa Glu	gaa Glu	cta Leu 240	aag Lys	gaa Glu	aaa Lys	tat Tyr	aaa Lys 245	gaa Glu	ctc Leu	acc Thr	833
gaa Glu	cag Gln 250	cag Gln	ctc Leu	cca Pro	ggc Gly	gca Ala 255	ctt Leu	cct Pro	cct Pro	gaa Glu	tgt Cys 260	acc Thr	ccc Pro	aac Asn	ata Ile	881
gat Asp 265	gga Gly	cca Pro	aat Asn	gct Ala	aaa Lys 270	tct Ser	gtt Val	cag Gln	aga Arg	gag Glu 275	caa Gln	agc Ser	tta Leu	cac His	tcc Ser 280	929
ttt Phe	cat His	acg Thr	ctt Leu	ttc Phe 285	tgt Cys	agg Arg	cga Arg	tgt Cys	ttt Phe 290	aaa Lys	tat Tyr	gac Asp	tgc Cys	ttc Phe 295 ·	Leu	977

															gaa Glu	1025
															ttg Leu	1073
						gct Ala 335										1121
						gga Gly									aat Asn 360	1169
						acc Thr										1217
gat Asp	aca Thr	gac Asp	agt Ser 380	gat Asp	agg Arg	gaa Glu	gca Ala	385 385	act Thr	gaa Glu	acg Thr	gl ^A aaa	gga Gly 390	gag Glu	aac Asn	1265
						gag Glu										1313
						caa Gln 415										1361
Glu 425	Pro	Pro	Glu	Asn	Val 430	gag Glu	Trp	Ser	Gly	Ala 435	Glu	Ala	Ser	Met	Phe 440	1409
Arg	Val	Leu	Ile	Gly 445	Thr	tac Tyr	Tyr	Asp	Asn 450	Phe	Cys	Ala	Ile	Ala 455	Arg	1457
tta Leu	Ile	gj gaa	acc Thr 460	aaa Lys	aca Thr	tgt Cys	aga Arg	cag Gln 465	gtg Val	tat Tyr	gag Glu	ttt Phe	aga Arg 470	gtc Val	aaa Lys	1505
Glu	Ser	Ser 475	Ile	Ile	Ala	cca Pro	Ala 480	Pro	Ala	Glu	Asp	Val 485	Āsp	Thr	Pro	1553
cca Pro	agg Arg 490	aaa Lys	aag Lys	aag Lys	agg Arg	aaa Lys 495	cac His	cgg Arg	ttg Leu	tgg Trp	gct Ala 500	gca Ala	cac His	tgc Cys	aga Arg	1601
						gac Asp										1649
caa Gln	ccc Pro	tgt Cys	gat Asp	cat His 525	cca Pro	cgg Arg	cag Gln	cct Pro	tgt Cys 530	gac Asp	agt Ser	tcg Ser	tgc Cys	cct Pro 535	tgt Cys	1697
gtg Val	ata Ile	gca Ala	caa Gln	aat Asn	ttt Phe	tgt Cys	gaa Glu	aag Lys	ttt Phe	tgt Cys	caa Gln	tgt Cys	agt Ser	tca Ser	gag Glu	1745

.:

550 540 545 1793 tgt caa aac cgc ttt ccg gga tgc cgc tgc aaa gca cag tgc aac acc Cys Gln Asn Arg Phe Pro Gly Cys Arg Cys Lys Ala Gln Cys Asn Thr aaq caq tqc ccq tqc tac ctq qct qtc cqa qaq tgt qac cct qac ctc 1841 Lys Gln Cys Pro Cys Tyr Leu Ala Val Arg Glu Cys Asp Pro Asp Leu tgt ctt act tgt gga gcc gct gac cat tgg gac agt aaa aat gtg tcc 1889 Cys Leu Thr Cys Gly Ala Ala Asp His Trp Asp Ser Lys Asn Val Ser 585 590 595 600 tgc aag aac tgc agt att cag cgg ggc tcc aaa aag cat cta ttg ctg 1937 Cys Lys Asn Cys Ser Ile Gln Arg Gly Ser Lys Lys His Leu Leu Leu gca cca tct gac gtg gca ggc tgg ggg att ttt atc aaa gat cct gtg 1985 Ala Pro Ser Asp Val Ala Gly Trp Gly Ile Phe Ile Lys Asp Pro Val 620 625 cag aaa aat gaa ttc atc tca gaa tac tgt gga gag att att tct caa 2033 Gln Lys Asn Glu Phe Ile Ser Glu Tyr Cys Gly Glu Ile Ile Ser Gln 635 640 645 gat gaa gct gac aga aga ggg aaa gtg tat gat aaa tac atg tgc agc 2081 Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr Asp Lys Tyr Met Cys Ser 655 ttt ctg ttc aac ttg aac aat gat ttt gtg gtg gat gca acc cgc aag Phe Leu Phe Asn Leu Asn Asn Asp Phe Val Val Asp Ala Thr Arg Lys 2129 665 670 675 ggt aac aaa att cgt ttt gca aat cat tcg gta aat cca aac tgc tat 2177 Gly Asn Lys Ile Arg Phe Ala Asn His Ser Val Asn Pro Asn Cys Tyr 685 690 gca aaa gtt atg atg gtt aac ggt gat cac agg ata ggt att ttt gcc 2225 Ala Lys Val Met Met Val Asn Gly Asp His Arg Ile Gly Ile Phe Ala 705 aag aga gcc atc cag act ggc gaa gag ctg ttt ttt gat tac aga tac 2273 Lys Arg Ala Ile Gln Thr Gly Glu Glu Leu Phe Phe Asp Tyr Arg Tyr 720 age cag get gat gee etg aag tat gte gge ate gaa aga gaa atg gaa 2321 Ser Gln Ala Asp Ala Leu Lys Tyr Val Gly Ile Glu Arg Glu Met Glu 735 atc cct tga catctgctac ctcctcccc tcctctgaaa cagctgcctt . 2370 Ile Pro 745 agcttcagga acctcgagta ctgtgggcaa tttagaaaaa gaacatgcag tttgaaattc 2430 tgaatttgca aagtactgta agaataattt atagtaatga gtttaaaaat caacttttta 2490 ttgccttctc accagctgca aagtgttttg taccagtgaa tttttgcaat aatgcagtat 2550 ggtacatttt tcaactttga ataaagaata cttgaacttg tcaaaaaaaa 2600

<210> 2

<211> 746

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Gln Thr Gly Lys Lys Ser Glu Lys Gly Pro Val Cys Trp Arg

1 10 15

Lys Arg Val Lys Ser Glu Tyr Met Arg Leu Arg Gln Leu Lys Arg Phe 20 25 30

Ile Leu Glu Arg Thr Glu Ile Leu Asn Gln Glu Trp Lys Gln Arg Arg 50 55 60

Ile Gln Pro Val His Ile Leu Thr Ser Val Ser Ser Leu Arg Gly Thr 65 70 75 80

Arg Glu Cys Ser Val Thr Ser Asp Leu Asp Phe Pro Thr Gln Val Ile 85 90 95

Pro Leu Lys Thr Leu Asn Ala Val Ala Ser Val Pro Ile Met Tyr Ser 100 105 110

Trp Ser Pro Leu Gln Gln Asn Phe Met Val Glu Asp Glu Thr Val Leu 115 120 125

His Asn Ile Pro Tyr Met Gly Asp Glu Val Leu Asp Gln Asp Gly Thr 130 135 140

Phe Ile Glu Glu Leu Ile Lys Asn Tyr Asp Gly Lys Val His Gly Asp 145 150 155 160

Arg Glu Cys Gly Phe Ile Asn Asp Glu Ile Phe Val Glu Leu Val Asn 165 170 175

Ala Leu Gly Gln Tyr Asn Asp Asp Asp Asp Asp Asp Gly Asp Asp 180 185 190

Pro Glu Glu Arg Glu Glu Lys Gln Lys Asp Leu Glu Asp His Arg Asp 195 200 205

Asp Lys Glu Ser Arg Pro Pro Arg Lys Phe Pro Ser Asp Lys Ile Phe 210 215 220

Glu Ala Ile Ser Ser Met Phe Pro Asp Lys Gly Thr Ala Glu Glu Leu 230 Lys Glu Lys Tyr Lys Glu Leu Thr Glu Gln Gln Leu Pro Gly Ala Leu 250 Pro Pro Glu Cys Thr Pro Asn Ile Asp Gly Pro Asn Ala Lys Ser Val 260 265 Gln Arg Glu Gln Ser Leu His Ser Phe His Thr Leu Phe Cys Arg Arg 280 Cys Phe Lys Tyr Asp Cys Phe Leu His Pro Phe His Ala Thr Pro Asn Thr Tyr Lys Arg Lys Asn Thr Glu Thr Ala Leu Asp Asn Lys Pro Cys 315 Gly Pro Gln Cys Tyr Gln His Leu Glu Gly Ala Lys Glu Phe Ala Ala 330 Ala Leu Thr Ala Glu Arg Ile Lys Thr Pro Pro Lys Arg Pro Gly Gly 340 345 350 Arg Arg Gly Arg Leu Pro Asn Asn Ser Ser Arg Pro Ser Thr Pro 355 Thr Ile Asn Val Leu Glu Ser Lys Asp Thr Asp Ser Asp Arg Glu Ala 370 Gly Thr Glu Thr Gly Gly Glu Asn Asn Asp Lys Glu Glu Glu Lys 385 390 395 400 Lys Asp Glu Thr Ser Ser Ser Glu Ala Asn Ser Arg Cys Gln Thr 405 410 Pro Ile Lys Met Lys Pro Asn Ile Glu Pro Pro Glu Asn Val Glu Trp 420 Ser Gly Ala Glu Ala Ser Met Phe Arg Val Leu Ile Gly Thr Tyr Tyr 440 Asp Asn Phe Cys Ala Ile Ala Arg Leu Ile Gly Thr Lys Thr Cys Arg

Gln Val Tyr Glu Phe Arg Val Lys Glu Ser Ser Ile Ile Ala Pro Ala

Pro Ala Glu Asp Val Asp Thr Pro Pro Arg Lys Lys Lys Arg Lys His 485 490 495

Arg Leu Trp Ala Ala His Cys Arg Lys Ile Gln Leu Lys Lys Asp Gly 500 505 510

Ser Ser Asn His Val Tyr Asn Tyr Gln Pro Cys Asp His Pro Arg Gln 515 520 525

Pro Cys Asp Ser Ser Cys Pro Cys Val Ile Ala Gln Asn Phe Cys Glu 530 540

Lys Phe Cys Gln Cys Ser Ser Glu Cys Gln Asn Arg Phe Pro Gly Cys 545 550 555

Arg Cys Lys Ala Gln Cys Asn Thr Lys Gln Cys Pro Cys Tyr Leu Ala 565 570 575

Val Arg Glu Cys Asp Pro Asp Leu Cys Leu Thr Cys Gly Ala Ala Asp
580 585 590

His Trp Asp Ser Lys Asn Val Ser Cys Lys Asn Cys Ser Ile Gln Arg 595 600 605

Gly Ser Lys Lys His Leu Leu Leu Ala Pro Ser Asp Val Ala Gly Trp
610 620

Gly Ile Phe Ile Lys Asp Pro Val Gln Lys Asn Glu Phe Ile Ser Glu 625 630 635 640

Tyr Cys Gly Glu Ile Ile Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys 645 650 655

Val Tyr Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp 660 665 670

Phe Val Val Asp Ala Thr Arg Lys Gly Asn Lys Ile Arg Phe Ala Asn 675 680 685

His Ser Val Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Asn Gly 690 695 700

Asp His Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Thr Gly Glu 705 710 715 720

Glu Leu Phe Phe Asp Tyr Arg Tyr Ser Gln Ala Asp Ala Leu Lys Tyr

725 730 735

Val Gly Ile Glu Arg Glu Met Glu Ile Pro 740 745

<210> <211> 2732 <212> DNA <213> Homo sapiens <220> <221> 5'UTR <222> (1)..(44) <220> <221> CDS <222> (45)..(1283) <220> <221> 3'UTR <222> (1284) . . (2732) <400> 3 tegegaggee ggetaggeee gaatgtegtt ageegtgggg aaag atg geg gaa aat 56 Met Ala Glu Asn tta aaa ggc tgc agc gtg tgt tgc aag tct tct tgg aat cag ctg cag 104 Leu Lys Gly Cys Ser Val Cys Cys Lys Ser Ser Trp Asn Gln Leu Gln gac etg tge ege etg gee aag ete tee tge eet gee ete ggt ate tet 152 Asp Leu Cys Arg Leu Ala Lys Leu Ser Cys Pro Ala Leu Gly Ile Ser aag agg aac ctc tat gac ttt gaa gtc gag tac ctg tgc gat tac aag 200 Lys Arg Asn Leu Tyr Asp Phe Glu Val Glu Tyr Leu Cys Asp Tyr Lys aag atc cgc gaa cag gaa tat tac ctg gtg aaa tgg cgt gga tat cca 248 Lys Ile Arg Glu Gln Glu Tyr Tyr Leu Val Lys Trp Arg Gly Tyr Pro gac toa gag age ace tgg gag eea egg eag aat ete aag tgt gtg egt 296 Asp Ser Glu Ser Thr Trp Glu Pro Arg Gln Asn Leu Lys Cys Val Arg 70 atc etc aag cag tte cae aag gae tta gaa agg gag etg etc egg egg 344 Ile Leu Lys Gln Phe His Lys Asp Leu Glu Arg Glu Leu Leu Arg Arg 90 95 100 cac các egg tea aag ace eec egg cac etg gac eea age ttg gee aac 392 His His Arg Ser Lys Thr Pro Arg His Leu Asp Pro Ser Leu Ala Asn 105 tac ctg gtg cag aag gcc aag cag agg cgg gcg ctc cgt cgc tgg gag 440 Tyr Leu Val Gln Lys Ala Lys Gln Arg Arg Ala Leu Arg Arg Trp Glu

4

and it is made to the course of the course o

: .

									-9-									
				gcc Ala												48	38	
			_	ctg Leu	_			_		_						53	36	
gag Glu 165	tac Tyr	cgt Arg	gtt Val	ggt Gly	gag Glu 170	ggc Gly	atc Ile	acc Thr	ctc Leu	aac Asn 175	cag Gln	gtg Val	gct Ala	gtg Val	ggc Gly 180	58	34	
_		_	_	gac Asp 185	_	_		_					_	_	_	63	32	
				cac His												68	30	
				ctg Leu												72	28	
				cca Pro												77	76	
	_			cgg Arg	_	_	_		_				_	_		82	24	
				cgc Arg 265												87		
				gag Glu												92	20	
_		_		tac Tyr			_	_	_				_			96	58	
				gcc Ala												101	.6	
				aac Asn												106	54	
				ccc Pro 345												111	.2	
_				ctc Leu			_			_			_			116	60	
				acc Thr												120	8	

385

2323

2383

2443

2503

2563

2623

2683

2732

380

cct ggc tcc cct aag aag cgg gtc cgt att gaa tgc aag tgt ggg act 1256 Pro Gly Ser Pro Lys Lys Arg Val Arg Ile Glu Cys Lys Cys Gly Thr 390 gag tcc tgc cgc aaa tac ctc ttc tag cccttagaag tctgaggcca 1303 Glu Ser Cys Arg Lys Tyr Leu Phe 405 410 gactgactga gggggcctga agctacatgc acctccccca ctgctgccct cctgtcgaga 1363 atgactgcca gggcctcgcc tgcctccacc tgcccccacc tgctcctacc tgctctacgt 1423 teagggetgt ggccgtggtg aggaccgact ceaggagtee cettteeetg teecageeee 1483 atctgtgggt tgcacttaca aacccccacc caccttcaga aatagttttt caacatcaag 1543 actototgto gttgggatto atggootatt aaggaggtoo aaggggtgag toccaacoca 1603 gccccagaat atatttgttt ttgcacctgc ttctgcctgg agattgaggg gtctgctgca 1663 ggcctcctcc ctgctgcccc aaaggtatgg ggaagcaacc ccagagcagg cagacatcag 1723 aggecagagt geetageeeg acatgaaget ggtteeeeaa eeacagaaae tttgtaetag 1783 tgaaagaaag gggtccctgg cctacgggct gaggctggtt tctgctcgtg cttacagtgc 1843 tgggtagtgt tggccctaag agctgtaggg tctcttcttc agggctgcat atctgagaag 1903 tggatgccca catgccactg gaagggaagt gggtgtccat gggccactga gcagtgagag 1963 gaaggcagtg cagagctggc cagccctgga ggtaggctgg gaccaagctc tgccttcaca 2023 gtgcagtgaa ggtacctagg gctcttggga gctctgcggt tgctaggggc cctgacctgg 2083 ggtgtcatga ccgctgacac cactcagagc tggaaccaag atctagatag tccgtagata 2143 gcacttagga caagaatgtg cattgatggg gtggtgatga ggtgccaggc actaggtaga 2203 gcacctggtc cacgtggatt gtctcaggga agccttgaaa accacggagg tggatgccag 2263

gaaagggccc atgtggcaga aggcaaagta caggccaaga attgggggtg ggggagatgg

cttccccact atgggatgac gaggcgagag ggaagccctt gctgcctgcc attcccagac

cccagccctt tgtgctcacc ctggttccac tggtctcaaa agtcacctgc ctacaaatgt

acaaaaggcg aaggttetga tggetgeett geteettget eeceeaceee etgtgaggae

ttctctagga agtccttcct gactacctgt gcccagagtg cccctacatg agactgtatg

ccctgctatc agatgccaga tctatgtgtc tgtctgtgtg tccatcccgc cggccccca

gactaacctc caggcatgga ctgaatctgg ttctcctctt gtacacccct caaccctatg

cagcctggag tgggcatcaa taaaatgaac tgtcgactga aaaaaaaaa

<210> 4 <211> 412 <212> PRT

375

<213> Homo sapiens

<400> 4

Met Ala Glu Asn Leu Lys Gly Cys Ser Val Cys Cys Lys Ser Ser Trp

5 10 15

Asn Gln Leu Gln Asp Leu Cys Arg Leu Ala Lys Leu Ser Cys Pro Ala 20 25 30

Leu Gly Ile Ser Lys Arg Asn Leu Tyr Asp Phe Glu Val Glu Tyr Leu 35 40 45

Cys Asp Tyr Lys Lys Ile Arg Glu Gln Glu Tyr Tyr Leu Val Lys Trp 50 60

Arg Gly Tyr Pro Asp Ser Glu Ser Thr Trp Glu Pro Arg Gln Asn Leu 65 70 75 80

Lys Cys Val Arg Ile Leu Lys Gln Phe His Lys Asp Leu Glu Arg Glu 85 90 95

Leu Leu Arg Arg His His Arg Ser Lys Thr Pro Arg His Leu Asp Pro 100 105 110

Ser Leu Ala Asn Tyr Leu Val Gln Lys Ala Lys Gln Arg Arg Ala Leu 115 120 125

Arg Arg Trp Glu Gln Glu Leu Asn Ala Lys Arg Ser His Leu Gly Arg 130 135 140

Ile Thr Val Glu Asn Glu Val Asp Leu Asp Gly Pro Pro Arg Ala Phe 145 150 155 160

Val Tyr Ile Asn Glu Tyr Arg Val Gly Glu Gly Ile Thr Leu Asn Gln 165 170 175

Val Ala Val Gly Cys Glu Cys Gln Asp Cys Leu Trp Ala Pro Thr Gly 180 185 190

Gly Cys Cys Pro Gly Ala Ser Leu His Lys Phe Ala Tyr Asn Asp Gln
195 200 205

Gly Gln Val Arg Leu Arg Ala Gly Leu Pro Ile Tyr Glu Cys Asn Ser 210 215 220

Arg Cys Arg Cys Gly Tyr Asp Cys Pro Asn Arg Val Val Gln Lys Gly 225 230 235 240

Ile	Arg	Tyr	Asp	Leu 245	Cys	Ile	Phe	Arg	Thr 250	Asp	Asp	Gly	Arg	Gly 255	Trp		
Gly	Val	Arg	Thr 260	Leu	Glu	Lys	Ile	Arg 265	Lys	Asn	Ser	Phe	Val 270	Met	Glu		
Tyr	Val	Gly 275	Glu	Ile	Ile	Thr	Ser 280	Glu	Glu	Ala	Glu	Arg 285	Arg	Gly	Gln		
Ile	Tyr 290	Asp	Arg	Gln	Gly	Ala 295	Thr	Tyr	Leu	Phe	Asp 300	Leu	Asp	Tyr	Val		
Glu 305	Asp	Val	Tyr	Thr	Val 310	Asp	Ala	Ala	Tyr	Туг 315	Gly	Asn	Ile	Ser	His 320		
Phe	Val	Asn	His	Ser 325	Cys	Asp	Pro	Asn	Leu 330	Gln	Val	Tyr	Asn	Val 335	Phe		
Ile	Asp	Asn	Leu 340	Asp	Glu	Arg	Leu	Pro 345	Arg	Ile	Ala	Phe	Phe 350	Ala	Thr		
Arg	Thr	Ile 355	Arg.	Ala	Gly	Glu	Glu 360	Leu	Thr	Phe	Asp	Tyr 365	Asn	Met	Gln		
Val	Asp 370	Pro	Val	Asp	Met	Glu 375	Ser	Thr	Arg	Met	Asp 380	Ser	Asn	Phe	Gly		
Leu 385	Ala	Gly	Leu	Pro	Gly 390	Ser	Pro	Lys	Lys	Arg 395	Val	Arg	Ile	Glu	Cys 400		
Lys	Cys	Gly	Thr	Glu 405	Ser	Cys	Arg	Lys	Tyr 410	Leu	Phe						
<210 <211 <212 <213	> 4 > D	89 NA	sapi	ens							•						
<400 actc	_		gggc	ctca	ıg ag	cact	ggga	ctg	caag	gtg	gttt	cctq	ta a	aaac	tgcag		6(
															tgggg		20
cacc	ttca	ta a	agga	gtct	g tg	caga	agaa	cga	attc	att	tctg	aata	ct g	tggt	gagct	1	80
catc	tctc	ag g	atga	ggct	g at	cgac	gcgg	aaa	ggtc	tat	gaca	aata	ca t	gtcc	agctt	2	4 (
cctc	ttca	ac c	tcaa	taat	g at	tttg	tagt	gga	tgct	act	cgga	aagg	aa a	caaa	attcg	3	00
attt	gcaa	at c	atto	aat.a	a at	ccca	actq	tta	tacc	222	aata	agtc	cc a	otaa	cctaa	3	۲,

gaggtg	gggt gggggatgga	tgcctcttta	ctgtgatttc	cattcgttgt	tgaacatttt	420
ccttag	ctga gctatcttt	gtccaaagat	aatcatgatt	aatatctggt	atcattttag	480
gcccct	ctc			•		489
<210>	6					
<211>	20					
<212> <213>	DNA Artificial Sequ	ience				
<220>						
<223>	EcoRI Adaptor o	oligonucleot	ide			
<400>	6				•	
aattct	cgag ctcgtcgaca	·				20
0.1.0						
<210><211>	7 31					
<212>	DNA					
<213>	Drosophila mela	nogaster				
<400>	7					
actgaa	ttcg gctggggcat	ctttcttaag	g			31
<210>	8					
<211>	31					
<212>	DNA					
<213>	Drosophila mela	nogaster				
<400>	8					
actcta	gaca atttccattt	cacgctctat	g			31
<210>	9					
<211>	30					
	DNA					
<213>	Drosophila mela	nogaster.				
<400>	9		-			
atatag	tact tcaagtccat	tcaaaagagg				30
					•	
<210>	10					
<211><212>	29 DNA					
<213>	Drosophila mela	nogaster				
<400>	10	++--				
ccayyca	accg ttggtgctgt	ccaayaccg				29
<210>	11					
<211>	760				•	
<212>	PRT					
	Drosophila mela	nogaster				
.400.	11			~		

..:

Met Asn Ser Thr Lys Val Pro Pro Glu Trp Lys Arg Arg Val Lys Ser 1 $$ 10 $$ 15

Glu Tyr Ile Lys Ile Arg Gln Gln Lys Arg Tyr Lys Arg Ala Asp Glu 20 25 30

Ile Lys Glu Ala Trp Ile Arg Asn Trp Asp Glu His Asn His Asn Val 35 40 45

Gln Asp Leu Tyr Cys Glu Ser Lys Val Trp Gln Ala Lys Pro Tyr Asp 50 60

Pro Pro His Val Asp Cys Val Lys Arg Ala Glu Val Thr Ser Tyr Asn 65 70 75 80

Gly Ile Pro Ser Gly Pro Gln Lys Val Pro Ile Cys Asx Ile Asn Ala 85 90 95

Val Thr Pro Ile Pro Thr Met Tyr Thr Trp Ala Pro Thr Gln Gln Asn 100 105 110

Phe Met Val Glu Asp Glu Thr Val Leu His Asn Ile Pro Tyr Met Gly 115 120 125

Asp Glu Val Leu Asp Lys Asp Gly Lys Phe Ile Glu Glu Leu Ile Lys 130 135 140

Asn Tyr Asp Gly Lys Val His Gly Asp Lys Asp Pro Ser Phe Met Asp 145 150 155 160

Asp Ala Ile Phe Val Glu Leu Val His Ala Leu Met Arg Ser Tyr Ser 165 170 175

Lys Glu Leu Glu Glu Ala Ala Pro Ser Thr Ser Thr Ala Ile Lys Thr 180 185 190

Glu Pro Leu Ala Lys Ser Lys Gln Gly Glu Asp Asp Gly Val Val Asp 195 200 205

Val Asp Ala Asp Cys Glu Ser Pro Met Lys Leu Glu Lys Thr Glu Ser 210 215 220

Lys Gly Asp Leu Thr Asp Val Glu Lys Lys Glu Thr Glu Glu Pro Val 225 230 235 240

Glu Thr Glu Asp Ala Asp Val Lys Pro Ala Val Glu Glu Val Lys Asp 245 250 255

Lys Leu Pro Phe Pro Ala Pro Ile Ile Phe Gln Ala Ile Ser Ala Asn 260 265 270

Phe Pro Asp Lys Gly Thr Ala Gln Glu Leu Lys Glu Lys Tyr Ile Glu 275 280 285

Leu Thr Glu His Gln Asp Pro Glu Arg Pro Gln Glu Cys Thr Pro Asn 290 295 300

Ile Asp Gly Ile Lys Ala Glu Ser Val Ser Arg Glu Arg Thr Met His 305 310 . 315 320

Ser Phe His Thr Leu Pro Cys Arg Arg Cys Phe Lys Tyr Asp Cys Phe 325 330 335

Leu His Arg Leu Gln Gly His Ala Gly Pro Asn Leu Gln Lys Arg Arg 340 345 350

Tyr Pro Glu Leu Lys Pro Phe Ala Glu Pro Cys Ser Asn Ser Cys Tyr 355 360 365

Met Leu Ile Asp Gly Met Lys Glu Lys Leu Ala Ala Asp Ser Lys Thr 370 375 380

Pro Pro Ile Asp Ser Cys Asn Glu Ala Ser Ser Glu Asp Ser Asn Asp 385 390 395 400

Ser Asn Ser Gln Phe Ser Asn Lys Asp Phe Asn His Glu Asn Ser Lys
405
410
415

Asp Asn Gly Leu Thr Val Asn Ser Ala Ala Val Ala Glu Ile Asn Ser 420 425 430

Ile Met Ala Gly Met Met Asn Ile Thr Ser Thr Gln Cys Val Trp Thr 435 440 445

Gly Ala Asp Gln Ala Leu Tyr Arg Val Leu His Lys Val Tyr Leu Lys 450 455 460

Asn Tyr Cys Ala Ile Ala His Asn Met Leu Thr Lys Thr Cys Arg Gln 465 470 475 480

Val Tyr Glu Phe Ala Gln Lys Glu Asp Ala Glu Ser Phe Ser Glu Asp 485 490 495

Leu Arg Gln Asp Phe Thr Pro Pro Arg Lys Lys Lys Lys Gln Arg

the second control of the second control of

500 505 510

Leu Trp Ser Leu His Cys Arg Lys Ile Gln Leu Lys Lys Asp Ser Ser 520 Ser Asn His Val Tyr Asn Tyr Thr Arg Cys Asp His Pro Gly His Pro 530 535 540 Cys Asp Met Asn Cys Ser Cys Ile Gln Thr Gln Asn Phe Cys Glu Lys 545 550 555 Phe Cys Asn Cys Ser Ser Asp Cys Gln Asn Arg Phe Pro Gly Cys Arg 565 570 Cys Lys Ala Gln Cys Asn Thr Lys Gln Cys Pro Cys Tyr Leu Ala Val Arg Glu Cys Asp Pro Asp Leu Cys Gln Ala Cys Gly Ala Asp Gln Phe 600 Lys Leu Thr Lys. Ile Thr Cys Lys Asn Val Cys Val Gln Arg Gly Leu 615 620 His Lys His Leu Leu Met Ala Pro Ser Asp Ile Ala Gly Trp Gly Ile 630 Phe Leu Lys Glu Gly Ala Gln Lys Asn Glu Phe Ile Ser Glu Tyr Cys Gly Glu Ile Ile Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr 665 Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp Phe Val Val Asp Ala Thr Arg Lys Gly Asn Lys Ile Arg Phe Ala Asn His Ser 690 695 Ile Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Thr Gly Asp His 705 710 Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Pro Gly Glu Glu Leu 725 Phe Phe Asp Tyr Arg Tyr Gly Pro Thr Glu Gln Leu Lys Phe Val Gly

745

740

Ile Glu Arg Glu Met Glu Ile Val 755 760

<210> 12

<211> 134

<212> PRT

<213> Homo sapiens

<400> 12

Ser Pro Ile His Gly Arg Gly Leu Phe Cys Lys Arg Asn Ile Asp Ala 1 5 10 15

Gly Glu Met Val Ile Glu Tyr Ala Gly Asn Val Ile Arg Ser Ile Gln 20 25 30

Thr Asp Lys Arg Glu Lys Tyr Tyr Asp Ser Lys Gly Ile Gly Cys Tyr 35 40 45

Met Phe Arg Ile Asp Asp Ser Glu Val Val Asp Ala Thr Met His Gly 50 55 60

Asn Arg Ala Arg Phe Ile Asn His Ser Cys Glu Pro Asn Cys Tyr Ser 65 70 75 80

Arg Val Ile Asn Ile Asp Gly Gln Lys His Ile Val Ile Phe Ala Met 85 90 95

Arg Lys Ile Tyr Arg Gly Glu Glu Leu Thr Tyr Asp Tyr Lys Phe Pro 100 105 110

Ile Glu Asp Ala Ser Asn Lys Leu Pro Cys Asn Cys Gly Ala Lys Lys 115 120 125

Cys Arg Lys Phe Leu Asn 130

<210> 13

<211> 132

<212> PRT

<213> Drosophila melanogaster

<400> 13

Ser His Ile His Gly Arg Gly Leu Tyr Cys Thr Lys Asp Ile Glu Ala 5 10 15

Gly Glu Met Val Ile Glu Tyr Ala Gly Glu Leu Ile Arg Ser Thr Leu
20 25 30

Thr Asp Lys Arg Glu Arg Tyr Tyr Asp Ser Arg Gly Ile Gly Cys Tyr 35 40 45

Met Phe Lys Ile Asp Asp Asn Leu Val Val Asp Ala Thr Met Arg Gly 50 55 60

Asn Ala Ala Arg Phe Ile Asn His Cys Cys Glu Pro Asn Cys Tyr Ser 65 70 75 80

Lys Val Val Asp Ile Leu Gly His Lys His Ile Ile Ile Phe Ala Val 85 90 95

Arg Arg Ile Val Gln Gly Glu Glu Leu Thr Tyr Asp Tyr Lys Phe Pro 100 105 110

Phe Glu Asp Glu Lys Ile Pro Cys Ser Cys Gly Ser Lys Arg Cys Arg 115 120 125

Lys Tyr Leu Asn 130

<210> 14

<211> 133

<212> PRT

<213> Caenorhabditis elegans

<400> 14

Ser Arg Ile His Gly Trp Gly Leu Tyr Ala Met Glu Ser Ile Ala Pro 1 5 10 15

Asp Glu Met Ile Val Glu Tyr Ile Gly Gln Thr Ile Arg Ser Leu Val 20 25 30

Ala Glu Glu Arg Glu Lys Ala Tyr Glu Arg Arg Gly Ile Gly Ser Ser 35 40 45

Tyr Leu Phe Arg Ile Asp Leu His His Val Ile Asp Ala Thr Lys Arg 50 55 60

Gly Asn Phe Ala Arg Phe Ile Asn His Ser Cys Gln Pro Asn Cys Tyr 65 70 75 80

Ala Lys Val Leu Thr Ile Glu Gly Glu Lys Arg Ile Val Ile Tyr Ser 85 90 95

Arg Thr Ile Ile Lys Lys Gly Glu Glu Ile Thr Tyr Asp Tyr Lys Phe 100 105 110

Pro Ile Glu Asp Asp Lys Ile Asp Cys Leu Cys Gly Ala Lys Thr Cys 115 120 125

Arg Gly Tyr Leu Asn 130

<210> 15

<211> 136

<212> PRT

<213> Saccharomyces cerevisiae

<400> 15

Ser Ala Ile His Asn Trp Gly Leu Tyr Ala Leu Asp Ser Ile Ala Ala 1 5 10 15

Lys Glu Met Ile Ile Glu Tyr Val Gly Glu Arg Ile Arg Gln Pro Val 20 25 30

Ala Glu Met Arg Glu Lys Arg Tyr Leu Lys Asn Gly Ile Gly Ser Ser 35 40 45

Tyr Leu Phe Arg Val Asp Glu Asn Thr Val Ile Asp Ala Thr Lys Lys 50 55 60

Gly Gly Ile Ala Arg Phe Ile Asn His Cys Cys Asp Pro Asn Cys Thr 65 70 75 80

Ala Lys Ile Ile Lys Val Gly Gly Arg Arg Ile Val Ile Tyr Ala 85 90 95

Leu Arg Asp Ile Ala Ala Ser Glu Glu Leu Thr Tyr Asp Tyr Lys Phe
100 105 110

Glu Arg Glu Lys Asp Asp Glu Glu Arg Leu Pro Cys Leu Cys Gly Ala 115 120 125

Pro Asn Cys Lys Gly Phe Leu Asn 130 135

<210> 16

<211> 429

<212> PRT

<213> Drosophila melanogaster

<400> 16

Met Gly Val Ile Ala Lys Arg Pro Pro Lys Gly Glu Tyr Val Val Glu

5 10 15

Arg Ile Glu Cys Val Glu Asn Asp Gln Tyr Gln Pro Val Phe Phe Val 20 . 25 30

Lys Trp Leu Gly Tyr His Asp Ser Glu Asn Thr Trp Glu Ser Leu Ala 35 40 45

Asn Val Ala Asp Cys Ala Glu Met Glu Lys Phe Val Glu Arg His Gln 50 55 60

Gln Leu Tyr Glu Thr Tyr Ile Ala Lys Ile Thr Thr Glu Leu Glu Lys 65 70 75 80

Gln Leu Glu Ala Leu Pro Leu Met Glu Asn Ile Thr Val Ala Glu Val 85 90 95

Asp Ala Tyr Glu Pro Leu Asn Leu Gln Ile Asp Leu Ile Leu Leu Ala 100 105 110

Gln Tyr Arg Ala Ala Gly Ser Arg Ser Gln Arg Glu Pro Gln Lys Ile 115 120 125

Gly Glu Arg Ala Leu Lys Ser Met Gln Ile Lys Arg Ala Gln Phe Val 130 135 140

Arg Arg Lys Gln Leu Ala Asp Leu Ala Leu Phe Glu Lys Arg Met Asn 145 150 155 160

His Val Glu Lys Pro Ser Pro Pro Ile Arg Val Glu Asn Asn Ile Asp 165 170 175

Leu Asp Thr Ile Asp Ser Asn Phe Met Tyr Ile His Asp Asn Ile Ile 180 185 190

Gly Lys Asp Val Pro Lys Pro Glu Ala Gly Ile Val Gly Cys Lys Cys 195 200 205

Thr Glu Asp Thr Glu Glu Cys Thr Ala Ser Thr Lys Cys Cys Ala Arg 210 215 220

Phe Ala Gly Glu Leu Phe Ala Tyr Glu Arg Ser Thr Arg Arg Leu Arg 225 230 · 235 240

Leu Arg Pro Gly Ser Ala Ile Tyr Glu Cys Asn Ser Arg Cys Ser Cys

Asp Ser Ser Cys Ser Asn Arg Leu Val Gln His Gly Arg Gln Val Pro 260 265 270

Leu Val Leu Phe Lys Thr Ala Asn Gly Ser Gly Trp Gly Val Arg Ala 275 280 285

Ala Thr Ala Leu Arg Lys Gly Glu Phe Val Cys Glu Tyr Ile Glu Glu 290 295 300

Ile Ile Thr Ser Asp Glu Ala Asn Glu Arg Gly Lys Ala Tyr Asp Asp 305 310 315 320

Asn Gly Arg Thr Tyr Leu Phe Asp Leu Asp Tyr Asn Thr Ala Gln Asp 325 330 335

Ser Glu Tyr Thr Ile Asp Ala Ala Asn Tyr Gly Asn Ile Ser His Phe 340 345 350

Ile Asn His Ser Cys Asp Pro Asn Leu Ala Val Phe Pro Cys Trp Ile 355 360 365

Glu His Leu Asn Val Ala Leu Pro His Leu Val Phe Phe Thr Leu Arg 370 375 380

Pro Ile Lys Ala Gly Glu Glu Leu Ser Phe Asp Tyr Ile Arg Ala Asp 385 390 395 400

Asn Glu Asp Val Pro Tyr Glu Asn Leu Ser Thr Ala Val Arg Val Glu
405 410 415

Cys Arg Cys Gly Arg Asp Asn Cys Arg Lys Val Leu Phe 420 425

<210> 17

<211> 166

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ala Lys Met Gly Trp Gly Val Arg Ala Leu Gln Thr Ile Pro Gln

5 10 15

Gly Thr Phe Ile Cys Glu Tyr Val Gly Glu Leu Ile Ser Asp Ala Glu 20 25 30

Ala Asp Val Arg Glu Asp Asp Ser Tyr Leu Phe Asp Leu Asp Asn Lys
35 40 45

Asp Gly Glu Val Tyr Cys Ile Asp Ala Arg Tyr Tyr Gly Asn Ile Ser 50 55 60

Arg Phe Ile Asn His Leu Cys Asp Pro Asn Ile Ile Pro Val Arg Val 65 70 75 80

Phe Met Leu His Gln Asp Leu Arg Phe Pro Arg Ile Ala Phe Phe Ser 85 90 95

Ser Arg Asp Ile Arg Thr Gly Glu Glu Leu Gly Phe Asp Tyr Gly Asp 100 105 110

Arg Phe Trp Asp Ile Lys Ser Lys Tyr Phe Thr Cys Gln Cys Gly Ser 115 120 125

Glu Lys Cys Lys His Ser Ala Glu Ala Ile Ala Leu Glu Gln Ser Arg 130 135 140

Leu Ala Arg Leu Asp Pro His Pro Glu Leu Leu Pro Glu Leu Gly Ser 145 150 155 160

Leu Pro Pro Val Asn Thr 165

<210> 18

<211> 139

<212> PRT

<213> Homo sapiens

<400> 18

Thr Gln Asn Lys Gly Trp Gly Ile Arg Cys Leu Asp Asp Ile Ala Lys

5 10 15

Gly Ser Phe Val Cys Ile Tyr Ala Gly Lys Ile Leu Thr Asp Asp Phe 20 25 30

Ala Asp Lys Glu Gly Leu Glu Met Gly Asp Glu Tyr Phe Ala Asn Leu 35 40 45

Asp His Ile Glu Ser Val Glu Tyr Ile Ile Asp Ala Lys Leu Glu Gly 50 55 60

Asn Leu Gly Arg Tyr Leu Asn His Ser Cys Ser Pro Asn Leu Phe Val 65 70 75 80

Gln Asn Val Phe Val Asp Thr His Asp Leu Arg Phe Pro Trp Val Ala 85 90 95

Phe Phe Ala Ser Lys Arg Ile Arg Ala Gly Thr Glu Leu Thr Trp Asp 100 105 110

1

. . .

```
Tyr Asn Tyr Glu Val Gly Ser Val Glu Gly Lys Glu Leu Leu Cys Cys
115 120 125
Cys Gly Ala Ile Glu Cys Arg Gly Arg Leu Leu
<210> 19
<211>
       20
<212> PRT
<213> Homo sapiens
<400> 19
Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro
Arg Lys Gln Leu
<210> 20
<211> 20
<212> PRT
<213> Homo sapiens
<400> 20
Met Gly Pro Arg Arg Arg Ser Arg Lys Pro Glu Ala Pro Arg Arg Arg
Ser Pro Ser Pro
            20
<210>
       21
<211>
       20
<212>
      PRT
<213> Rattus sp.
<400> 21
```

Met Ser Ser Arg Gly Gly Lys Lys Ser Thr Lys Thr Ser Arg Ser

Ala Lys Ala Gly 20